SEQUENCE LISTING

<110> Biogen Idec MA Inc. Prentice, Holly <120> HIGH EXPRESSION LOCUS VECTOR BASED ON FERRITIN HEAVY CHAIN GENE LOCUS <130> 2159.058PC01/EKS/LMB <140> PCT/US2003/033433 <141> 2003-10-22 <150> US 60/421,252 <151> 2002-10-24 <160> 41 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 563 <212> DNA <213> Rattus norvegicus <220> <221> CDS <222> (346)...(459) <400> 1 ageteagaga eccaagagee geeteacaat cacacagget ecteecegee caegeactge 60 tggcttgggc aacacgccta caggaagagg cggggctggg cggcccaccg cgctgattgg 120 ccggagcgcg cctgacgcag gatcccgcta taaagtgcgg cccgctggtc cctacgccag 180 acgttetege ccagagtege egeggtttee tgetteaaca gtgettgaac ggaaceeggt 240 getegacece teegacece greeggeege trtgageetg ageeettige aactregteg 300 ctccgccgct ccagcgtcgc ctccqcgcct cgtccaqccq ccatc atq acc acc qcq 357 Met Thr Thr Ala tet eec teg caa gtg ege cag aac tac cac cag gae teg gag get gee 405 Ser Pro Ser Gln Val Arg Gln Asn Tyr His Gln Asp Ser Glu Ala Ala 5 10 atc aac cgc cag atc aac ctg gag ttg tat gcc tcc tac gtc tat ctg 453 Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser Tyr Val Tyr Leu 30 35 tcc atg gtgagtgcgg cctggccttt gcgggggcgg aaagagggtg cggcctggcc 509 Ser Met tcccttgggc cacttggtga gctggcggag ggtgggttgg ggcgtggctg cggg 563 <210> 2 <211> 38 <212> PRT <213> Rattus norvegicus

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Tyr Phe Leu His Gln Ser His Glu Glu Arg Glu His Ala Glu Lys Leu

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gat ccc cac gtgagtatca gaaacacggg gtgagtggag atgatttgcc
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                                                           Leu Cys
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Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys
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Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu
tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt
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Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly
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85

80

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acactetttt ccaagtgcag tgcacacete attgcattca gcccgetete ccagteatea
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1399
1459
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														cct Pro 125		1816
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540

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ttgctgtggg gatcaataac aaataccctt tccatttaaa tctgctagcg gccgctgacg
                                                                       1320
tccccaaggc catgtgactt tactggtcac tgaggcagtg catgcatgtc aggctgcctt
                                                                       1380
tatcttttct ataagttgca ccaaaacatc tgcttaaaag ttctttaatt tgtaccattt
                                                                       1440
cttcaaataa agaattttgg tacccagctc ttgttgtgat tgaggatgag cgcaccagct
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tcccttgcgt cggctatact aaccacactg ca
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              Met Thr Thr Ala Ser Pro Ser Gln Val Arg Gln Asn Tyr
cac cag gac tcg gag gct gcc atc aac cgc cag atc aac ctg gag ttg
                                                                        99
His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu
                         20
tat gcc tcc tac gtc tat ctg tcc atg gtgagtgcgg cct
                                                                       139
Tyr Ala Ser Tyr Val Tyr Leu Ser Met
30
                     3.5
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<212> PRT
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Met Thr Thr Ala Ser Pro Ser Gln Val Arg Gln Asn Tyr His Gln Asp
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Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser
                                 25
                                                     30
Tyr Val Tyr Leu Ser Met
        35
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actttcagct gctagcggcc gcgctgacgt ccccaaggcc at
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acgtcagcgc ggccgctagc agctgaaagt ggaaagggta t
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                                                                         23
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gtcgaccaca gacgtcaacc gtt
                                                                         23
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